

### CDC7 Gene Structure

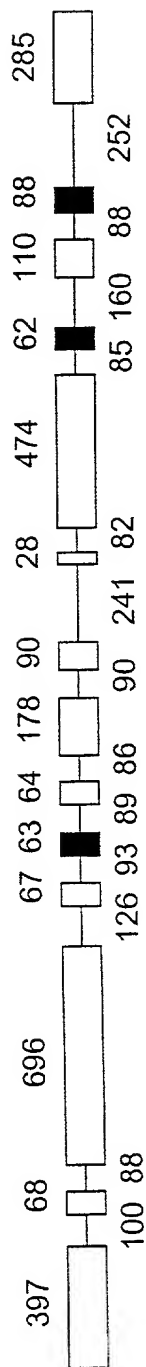


FIGURE 1

# CDC27A1 Gene Structure

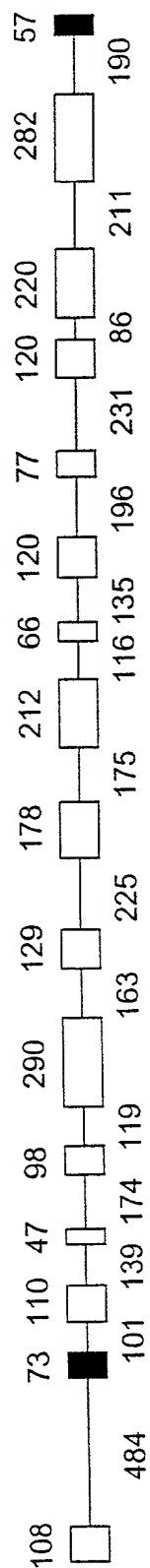


FIGURE 2

Fig. 3

1 ATGT CAGAAA ACTCGGAACCGCGTCAACTCGAGAATTCCTACA 60  
 TCTAAGTGTCTGTAACGTTACAGTCTTTTGAGCCTTGGCGCAGTTGAGCTCTTAAGATGT  
 M S E N S E P R Q L E N S T -  
 61 GCCGGAAGAGAGCTCATTCTCTTAGTCCCACCAATTCAGACGGCAACGACGACCTTAAC 120  
 CGGCCCTTCTCTCGAGTAAGGAGAATCAGGGTGGTTAAGTCTGCCGTTGCTGCTGGAATTG  
 A G R E L I P L S P T N S D G N D D L N -  
 121 TATCATCTGCATGCTTTTGGAGTTATCTCGTCTCCTACTTTCTTCTGGTCATCCAGAATCT 180  
 ATAGTAGACGTACGAAAACCTCAATAGAGCAGAGGATGAAAGAAGACCAGTAGGTCTTAGA  
 Y H L H A F E L S R L L L S S G H P E S -  
 181 GTTATAGATCTTTTCTTCAAAGTGTACATACTTCCAAGGTTCTCCTAATCTCGTCAAATAT 240  
 CAATATCTAGAAAGAAGTTTCAATGTATGAAGGTTCCAAGAGGATTAGAGCAGTTTATA  
 V I D L S S K C T V F Q G S P N L V K Y -  
 241 CTTTGCTCGATCCCTAATTCCTCTATTTCCCTTGGCGAAGATGGCTTCAGTGTGACTCTC 300  
 GAAACGAGCTAGGGATTAAAGAGGATAAAGGGAACGGCTTCTACCGAAGTGACACTGAGAG  
 L C S I P N S P I S L A E D G F T V T L -  
 301 TCGCCTGAGTCTCCCTCCGCTCCGGCTAGTTTCGCCCTGTAGTTTGGATTTCAGGAAAAT 360  
 AGCGGACTCAGAGGGAGGCGAGGCCGATCAAAGCGGACATCAAACCTAAACGTCCTTTTA  
 S P E S P S A P A S F A C S L D L Q E N -  
 361 GTTGTGTTAGAACAGTTTATGGATCCGAGATCTCTCAGGCTAAAGCATTCCAGAGAGAAT 420  
 CAACACAATCTTGTCAAATACCTAGGCTCTAGAGAGTGGATTTCGTAAGCTCTCTCTTA  
 V V L E Q F M D P R S L T L K H S R E N -  
 421 GCCGAACAAGAGGAGCTAGAGCTCATGCCATTGCCCAAAAGAAGTCGAAATGATGGAAAC 480  
 CGCCTTGTTCTCCTCGATCTCGAGTACGGTAACGGGTTTCTTCAGCTTTACTACCTTTG  
 A E Q E E L E L M P L P K R S R N D G N -

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481 43  
GATGTGAATTAATCTGCTAATAGATAGCGACCTTAACGACATCGAAGCTGTGCGCTGCGA 540  
CTACACCTTAATGAGACATTTATCTATCGTCTGGAATTGCTGTAGTCTTGAACACGACACCT  
43  
D V N Y S V I D S R E N D I R T V A C G -  
541 ACTATGCTTGGGACTATTTTATGCTCTTGAATCCCAAGCTTGGTCTTCAATTAAAGTGC 500  
TGATACGAACCCCTGATAAAATCGAGAACTTAGGGTTCGAAGCCAAAAGTTAAATTACGT  
T M L G T I L A L E S Q A S V F N L S A -  
601 TCTAACCGAGGAATAGAGGCTTTTGTTCAGATCATCAGCCTGGTCCGCGAGACATCCAT 560  
AGATTGGCTCCTTATCTCCGAAAACAAGTTCTAGTAGTCCGACCCGGGCTCTGAGGTTA  
S N R G I E A F V Q D E Q P G P Q T S N -  
661 GCTTCAGTGGATGTCAATCCTACACATCGGTTAGAGGAAAGCAAGAACGATTTGCCATCT 720  
CGAAGTCACCTACAGTTAGGATGTGTAGCCCAATCTCCTTTCTTCTGCTAAACGGTLAGA  
A S V D V N P T H R L E E S K N D L P S -  
721 COTCAGGAGGATGGATATTACGAGCGACCTGAAATTGGAGATTTCCAAATTGCTGACAC 780  
GGAGTCCCTCCTACCTATAATGCTCGCTGGACTTTAACCTCTAAAGGTTTAAACGCTGTG  
P Q E D G Y Y E R P E I G D F Q I A D N -  
781 CAAATATTAATCGAAGAAGGTGATGATAAAAAATAAGAAGGATCTCTTCCCTAAGGGAGAG 840  
GTTTATAATTAAGCTTCTTCCACTACTATTTTATTTCTTCTTCTAGAGAGGGGATCCCTCTC  
Q I L I E E G D D K N K K D L F P K G E -  
841 ATACAAACTGATTCTGTGCACTCCGATCCCGTTGCCTCATTCATGCCAACAGAAATGAG 900  
TATGTTTGAATAAGACACCTCAGGCTAGGGCAACCGAGTAACTACGGTTGTCTTTTACTC  
I Q T D S V Q S D P V A S L M P T E N E -  
901 TTAGAACCAGTGCAGATTGTGGATGACACTGAAGATCTACTTGTAGATGATCACACTGTA 960  
AATCTTGGTCACTCTAACACCTTACTGTGACTTCTAGATGAACATCTACTAGTGTGACAT  
L E P V Q I V D D T E D L L V D D H T V -  
961 GACATCGTTAGCACCCCTGACAGAGAGCTGCCCTTGAAGCCCTTCTGCTACAGAAGCTAAT 1020  
CTGTAGCAATCGTGGGCACTGTCTCTCGACCGCACTTTCGGAAGACGATGTCTTCGATTA  
D I V S T P D R E L P L K P S A T E A N -  
1021 CAAGATAAATCTTTGGTACAAAAAACTCTGGATCAATGCAAAATTGCCGGGAAACAGCAAA 1080  
GTTCTATTTAGAAACCATGTTTTTTTGAGACCTAGTTACGTTTAAACGGCCCTTTGTCTTT

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Q D K S L V Q K T L D Q C K L F G N S K -  
ACGTACAGCTGTTCCCTGAGATAAAACACACCAGAAAAGTAAAGTTATCCAGAAGAGG 1140  
TGCATGTCCGACAAGGGGACCTATTTTGTGTGGTCTTTTTCATTTCATAGGTCTCTCTCC  
T Y S C S P E I K H T R K S K V I Q K R -  
AAGCAGAATTTTAAACACCGTTTCGTCTTAAAGATCAGAAGCATCAGGCAAAGCATACACA 1200  
TTCGTCTTAAAAATTGTGGCAAGCAGAAATTTCTAGTCTTCTAGTCCGTTTTCGTATTGEGT  
K Q N F N T V R L K D Q K D Q A K H N T -  
ATTCCAGATTTTIGATTCTTACACTATTGTAGAGGAAGAGGTTTCAGTTGGCTACGGGATT 1250  
TAAGGTCTAAAACTAAGAATGTGATAACATCTCTCTTCCAAGTCCACCGATGCCCTAA  
I P D F D S Y T I V E E E G S G G Y G I -  
GTTTTATAAGGCAACGAGGAAAACCTGATGGACAGAGTTTGCATTTAAATGCCCCCATGTT 1320  
CAAATATTCCGTTGCTCCTTTTGACTACCTTGTCTCAACGTTAATTTACGGGAGTACAA  
V Y K A T R K T D G T E F A I K C P H V -  
GGCGCTCAGAAGTATTATGGAATAATGAAATCAGAATGCTGGAGCGTTTGGGGGAAA 1380  
CCGCGAGTCTTCATAATACACTTATTACTTTAGTCTTACGACCTCGCAAACCCCCCTTT  
G A Q K Y Y V N N E I R M L E R F G G K -  
AACTGTATAATAAAGCATGAAGGCTGTCTCAAGAATGGAGATTCTGATTGCATCATCTTT 1440  
TTGACATATTATTTTCGTACTTCCGACAGAGTTCTTACCTCTAAGACTAACGTAGTAGGAA  
N C I I K H E G C L K N G D S D C I I L -  
GAGCACCTTGAACATGACAGACCTGATTCAATGAAGAGAGAAATAGATGTGTATCAGCTG 1500  
CTCGTGGAACCTTGTACTGTCTGGACTAAGTAACTTCTCTCTTTATCTACACATAGTCGAC  
E E L E H D R P D S L K R E I D V Y Q L -  
CAGTGGTACGGCTACTGCAATGTTCAAAGCTCTATCGAGTCTGCATAAGCAGGGTGTGTT 1560  
GTCACCATGCCGATGACGTACAAGTTTTCGAGATAGCTCAGACGTATTCTTCCCACAACAA  
Q W Y G Y C M F K A L S S L H K Q G V V -  
CATAGGGATGTTAAGCCAGGAAACTTCTCTCTCTAGGAAGACCAACAAAGGCTATCTC 1620  
GTATCCCTACAAATTCGGTCTCTTGAAGGAGAAGAGATCTTCTGTTGTTTCCGATAGAG  
H R D V K P G N F L F S R K T N K G Y L -  
ATTGATTTTAACTTGGCATGATTGTCACCAGAAGTACAGAAGAGCAGATAAATCAAAA

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1621 ----- 1680  
TAACTAAAAATTGGACCGGTACCTTAAACGGTGGTCTTCTATGTCCTTCTCGTCTATTAGTTTT  
8|9 3|10  
I D F N L A M | D L H Q K Y R R A D | K S K -  
GCAGCTTCAGGTCTTCCCTACCGCCAGCAAGAACTTCATTCATTGGTTAAATCACTCCAT  
1681 ----- 1740  
CGTCCAGTCCAGAGGATGGCCGGTCTTCTTGTAGTATGTAACCAATTATAGTGAGCTA  
A A S G L P T A S K K E E T L V K S L D -  
GCGGTAAACCGAGGGACCAACAAACCTTCTCAGAAAACCTTAGCCCTAATAGTATCAG  
1741 ----- 1800  
CGCCATTGTTGGCTCCCTGGTGTGTTTGGGAAGAGTCTTTTGAAATCCGGATTATCATAGTTC  
A V N R G T N K P S Q K T L A P N S I K -  
AAAGCAGCGGGAAAGACAAGAGCTCGGAATGACATGACCAGATGGGAGAGACTCAATAGC  
1801 ----- 1860  
TTTCGTCCGCCCTTCTGTCTCTCGAGCCCTTACTGTACTGGTCTACCCCTCTCTGAGTTATCG  
K A A G K T R A R N D M T R W E R L N S -  
CAAGGGGCAGAAAGGTCTGGCTTAACTTCAGCTAAAGATGTGACCAAGCAAGGAACAAC  
1861 ----- 1920  
GTTCCCCCTCTTCCAGACCGAATTGAAGTCGATTTCTACACTGGTCTGTCTCTTGTG  
Q G A E G S G L T S A K D V T S T R N N -  
CCTTCAGGTGAAAAGAGAGAGAGCCCTTGGCATGTGATGGAAGAAAAGCGCTTTTAGAT  
1921 ----- 1980  
GGAAGTCCACTTTTCTTCTCTCTCGGAAACGGTACAGTACCTTCTTTTCGCGAAAATCTA  
P S G E K R R E P L P C H G R K A L L D -  
TTTCTGCAAGAGACAATGTCTGTCTCCAATTCGAAACCATGAAGTATCATCCAAAGCTCCT  
1981 ----- 2040  
AAAGACGTTCTCTGTACAGACAAGGTTAAGGTTTGGTACTTCATAGTAGGTTTCGAGGA  
F L Q E T M S V P I P N H E V S S K A P -  
ACGTCTATGAGAAAACGGGTAGCTGTCTCTTCCAGGGAAAGCTGAGAAGGAACCTTCTTTAT  
2041 ----- 2100  
TGCAGATACTCTTTTGGCCATCGACGAGAAGTCCCTTTTCACTCTTCTTGAAGAAATA  
T S M R K R V A A L P G K A E K E L L Y -  
CTGACCCCAATGCCACTGTGTCTTAAACGGTGGCCCTGAAGCAGGGGACGTAATTGAGAAG  
2101 ----- 2160  
GACTGGGGTTACGGTGAACAGAGATTGCCAGCCGGACTTCGTCCCTGCACTAACTCTTC  
10|11  
L T P M P L C S N G R P E A G | D V I E K -  
AAAGACGGTCTTTGCTCAGGAACCAAGGCTTCCGAGCTCCAGAGGTTTGTCTTCAGATCT  
2161 ----- 2220  
TTTCTGCCAGGAACGAGTCTTTGGTTTCCGAAGGCTCGAGGTCTCCAAACGAAGTCTAGA  
11|12  
K D G P C S G T K G F R A P E | V C F R S -

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2221 TGGCACCAGGACCTAAGATGACGCTGGGTCTGGCGGGAGTTA CTTTGTATACCTCATA 2280  
AACCTGGTTCCTGGATTCTATCTGCAACCGACGCGCCTCAATGAAACAATATGGAGTAT  
L H Q G E K I D V W S A G V T L L Y L I -  
2281 ATGGGAAGGACACCTTTCACTGGTGA CCGCTGAAC<sup>12/13</sup> GAACATAAAGGACATTGGCA CAACTA 2340  
TACCCCTTCCTGTGGAAAGTGACCACTGGGACTTGTCTGTATTTCCTGTAACTGTGTGAT  
M G R T P F T G D E E Q<sup>12/13</sup> N I K D I A Q L -  
2341 CGAGGCAGTGAAGAATTATGGGAAGTAGCCAGCTGCCCAACCGTGAATCCTCTTTCCCT 2400  
GCTCCGTCACTTCTTAATAACCTTCATCGGTTCGACCGTGTGGCACTTAGGAGAAAGGGA  
R G S E E L W E V A K L E N R E S S E P -  
2401 AAGGAATTATACGAGTCAAGGTACTTGAAGGGGATGGAGTTGAGAAAATGGTGCGAAGTC 2460  
TTCTTAATATGCTCAGTTCATGAACCTTCCCTACCTCAACTCTTTTACCAAGCTTGAG  
K<sup>13/14</sup> E L Y E S R Y L K G M E I R K W C E L -  
2461 AACACAAAACGCAGAGAGTTTCTAGACGTAATTCCACTATCGCTTCTTGACCTCGTTGAT 2520  
TTGTGTTTTGCGTCTCTCAAGATCTGCATTAAAGGTGATAGCGAAGAACTGGAGCAACTA  
N T K R R E F L D V I P L S L L D L V D -  
2521 AAATGTTTGACCGTTAACCCGAGGCGACGAATCAGCGCAGAGGATGCTCTCAAGCACGAC 2580  
TTTACAAACTGGCAATTGGGCTCCGCTGCTTAGTCCGCTCTCCTACGAGAGTTCTGTGCTG  
K C L T V N P R R R I S A E D A L K H D -  
2581 TTCTTCCATCCAGTACATGAACCCCTTAGAAACCAATGCTCCTTAAACAGCAGCCTACA 2640  
AAGAAGGTAGGTCACTACTTTGGGAATCTTTGGTTTACGAGGAATTTGTGCTGCGGATGT  
F F H P V H E T L R N Q M L L K Q Q P T -  
2641 GTGGTTGCTGACCGCAAGCCAAACTCTAAACTATTTACAATTGTAAAGTAAATAAG<sup>14/</sup> 2699  
CACCAACGACTGCCTCATTCGGTTTGAGATTTCATAAATGTTAACATTTTCATTTATTC  
V V A D A V S Q T L N Y L Q L \*

[illegible]

1 60  
CCGCTGTAATGTGTGTGTCGGAGGCCTCTTGTGTGTGTGTAGCTAACAGAGCAGTTAA  
61  
ATGATGGAGAATCTACTGGCGAATTGTGTCCAGAAAAACCTT  
120  
CCAGTAGTAGTAGTACTACTACCTCTTAGATGACCGCTTAACACAGGTCTTTTGGAA  
M M E N L L A N C V Q K N L  
AACCATTTTATGTTTACCAATGCTATCTTTCCTTTGCGAAGTTCTTCTCGCCCAATTTCCA  
121  
TTGGTAAAATACAGTGGTTACGATAGAAGGAAACGCTTGAAGAGAGCGGGTTAAAGGT  
N H F M F T N A I E L C E L L L A Q F P  
TCTGAGTGAACCTGCAATTGTTAGCCAGGTGTTACTTTCAGTAACAGTCAAGCTTATAGT  
181  
AGACTCCACTTGGACGTTAACAATCGGTCCACAATGAAGTCAATTTGTTCAGTTCCGAATATCA  
S E V N L Q L L A R C Y L S N S Q A Y S  
GCATATTATATCCTTAAAGGTTCAAAAAACGCTCAGTCTCGGTATTTTATTTTGCATTCTCA  
241  
CGTATAATATAGGAATTTCCAAGTTTTTTCGGGAGTCAGAGCCATAAATAAACGTAAGAGT  
A Y Y I L K G S K T P Q S R Y L F A F S  
TGCTTTAAGTTGGATCTTCTTGGAGAGGCTGAAGCTGCATTGTTTGGCCCTGTGAGATTAT  
301  
ACGAAATTTCAACCTAGAAGAACCTCTCCGACTTCCAGCTAACCAACGGGACACTTCTAATA  
C F K L D L L G E A E A A L L P C E D Y  
GCTGAAGAGTTTCTGTTGGTGCAGCTGGGCAATTATCTTCTTGGTCTTATATATAGATAT  
361  
CGACTTCTTCAAGGACCACCACTCGACCCGTAATAGAGAACAGAAATATATATCTATA  
A E E V P G G A A G H Y L L G L I Y R Y



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TCTGGGAGGAAGAACTGTTCAATACAACAGTTTAGGATGGCATTGTCATTTGATCCATTG  
421 ----- 480  
AGACCCCTCCTTCTTGACAAGTTATGTTGTCAAATCCTACCGTAACAGTAAACTAGGTAAC  
  
S G R K N C S I Q Q F R M A L S F D P L  
516  
TGTGGGAAGCATATGGAGAAGTTTGTAGTTTAGTTGCCGCTGAAGAAGCCTCAACAGTT  
481 ----- 540  
ACAACCCCTTCGTATACCTCTTGAAACATCAAATCCACGGCGACTTCTTCGGAGTTGTCAA  
516  
C W E A Y G E L C S L G A A E E A S T V  
  
TTCGGGAATGTTGCTTCCCAGCGTCTTAAAACTTGTGTAGAACAAGAATAAGCTTCTCA  
541 ----- 600  
AAGCCCTTACAACGAAGGGTTCGCAGAATTTTGAACACATCTTGTTCCTTATTCGAAGAGT  
  
E G N V A S Q R L K T C V E Q R I S F S  
  
GAAGGAGCAACCATAGACCAGATTACAGATTCTGATAAGGCCCTTAAAAGATACAGGTTTA  
601 ----- 660  
CTTCCTCGTTGGTATCTGGTCTAATGTCTAAGACTATTCGGGAATTTTCTATGTCCAAT  
  
E G A T I D Q I T D S D K A L K D T G L  
  
TCGCAAACAGAACACATTCCAGGAGAGAACCAACAGATCTGAAAATTATGCAGCAGCCT  
661 ----- 720  
AGCGTTTGTCTTGTGTAAGGTCCTCTCTTGGTTGTTCTAGACTTTTAATACGTCGTCGGA  
  
S Q T E H I P G E N Q Q D L K I M Q Q P  
  
GGAGATATTTCCACCAAATACTGACAGGCAACTTAGTACAAACGGATGGGACTTGAACACA  
721 ----- 780  
CCTCTATAAGGTGGTTTATGACTGTCCGTTGAATCATGTTTGCCTACCCCTGAACTTGTGT  
  
G D I P P N T D R Q L S T N G W D L N T  
617  
CCTTCTCCAGTGCTTTTACAGGTAATGGATGCTCCACCGCCTCTGCTTCTTAAGAATATG  
781 ----- 840  
GGAAGAGGTCACGAAAATGTCCATTACCTACGAGGTGGCGGAGACGAAGAATTCTTATAC  
617  
P S P V L L Q V M D A P P P L L L K N M  
  
CGTCGTCCAGCAGTGGAAGGATCTTTGATGTCTGTACATGGAGTGGTGTGCGTCCAAGA  
841 ----- 900  
GCAGCAGGTCGTCACCTTCCTAGAACTACAGACATGTACCTCACGCACACGCAGCTTCT  
  
R R P A V E G S L M S V H G V R V R R R

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7<sup>8</sup>  
901 AACTTTTTGTGAAGAATTGTCAGCAGAGGCTCAAGAAGAATCTGGGGCGCCGCCGTAGT 960  
-----  
TTGAAAAAATCACTTCTTAACAGTCGTCTCCGAGTTCTTCTTAGACCCCGCGCGGCATCA  
7<sup>8</sup>  
N F F S E E L S A E A Q E E S G R R R S  
GCTAGAATAGCAGCAAGGAAAAAGAATCCTATGTGCGCAGTCATTTCGAAAAAGATTCCCAT  
961 ----- 1020  
CGATCTTATCGTCGTTTCCTTTTCTTAGGATACAGCGTCAGTAAACCTTTTCTAAGGGTA  
A R I A A R K K N P M S Q S F G K D S H  
TGTTTACATCTTTTACCTTCCGAGTCAAACATATGCACCTTCTCTTTCCTTCGATGATTGGA  
1021 ----- 1080  
ACCAATGTAGAAAGTGAAGGCTCAGTTTGTATACGTGGAAGAGAAAGGAGCTTACTAACCT  
W L H L S P S E S N Y A P S L S S M I G  
8<sup>9</sup>  
1081 AAATGCAGAATCCAAAGCAGCAAAGAAGCGATTCTGTATACCGTTACTCTAAATGATCCA 1140  
-----  
TTTACGTCCTTAGGTTTTCGTCGTTTCTTCGCTAAGGACTATGGCAATGAGATTACTAGGT  
8<sup>9</sup>  
K C R I Q S S K E A I P D T V T L N D P  
GCAACGACGTCAGGCCAGTCTGTAAAGTGACACTGGAAGCTCTGTTGATGATGAGGAAAAG  
1141 ----- 1200  
CGTTGCTGCAGTCCGGTCAGACATTCACTGTGACCTTCGAGACAACTACTACTCTTTTTC  
A T T S G Q S V S D T G S S V D D E E K  
TCAAATCCTAGTGAATCTTCCCCGGATCGTTTTCAGCCTTATTTCTGGAATTTTCAAGAGTG  
1201 ----- 1260  
AGTTTAGCATCACTTAGAAGGGGCCTAGCAAAGTCGGAATAAAGACCTTAAAGTCTTCAC  
S N P S E S S P D R F S L I S G I S E V  
CTAGGCATTCTGAAAATTCTTGGAGATGGCCACAGGCATTTACATATGTACAAGTGTGAG  
1261 ----- 1320  
GATCCGTAAGACTTTTAAGAACCTCTACCGGTGTCCGTAAATGTATACATGTTTCACAGTC  
9  
L G I L K I L G D G H R H L H M Y K C Q  
9

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1321 GAAGCTTTTGGTCATATCAAAAGCTATCTCAGAAACATACAATACACACTGGGTTCTC 1380  
CTTCGAAACACCGTATAGTTTTCCGATAGAGTCTTTGTTATGTTATGTGTGACCCAGAG  
1381 E A L L A Y Q K L S Q K Q Y N T H W V L  
ATGCAGTTTGGAAAAGCATATTTTGGAGCTACAAGACTACTTCAACCGCTGACTCTTCTCTT  
TACGTCCACCTTTTTCGTATAAAACTCGATGTTCTGATGAAGTTGCGACTGAGAAGGAAA 1440  
M Q V G K A Y F E L Q D Y F N A D S S F  
ACTCTTGCTCATCAAAAGTATCCTTATGCTTTTGGGAAGGAATGGATACATACTCCACTGTT  
1441 TGAGAACGAGTAGTTTTCATAGGAATACGAAACCTTTCCTTACCTATGTATGAGGTGACAA 1500  
T L A H Q K Y P Y A L E G M D T Y S T V  
CTTTATCACCTGAAAGAAGAGATGAGGTTGGGCTATCTGGCTCAGGAACTGATTTTCAGTT  
1501 GAAATAGTGGACTTTTCTCTCTACTCCACCCGATAGACCGAGTCTTTGACTAAAGTCAA 1560  
L Y H L K E E M R L G Y L A Q E L I S V  
GATCGCTGTCTCCAGAATCCTGTTGTGTCAGTTGGGAAGTGTACAGTTTTCCTAAGGAT  
1561 CTAGCGGACAGAGGTCTTAGGACCAACGTCACCCCTTGACAATGTCAAACGCTTCTCTA 1620  
D R L S P E S W C A V G N C Y S L R K D  
CATGATACTGCTCTCAAAATGTTTTCAGAGAGCTATCCAACTGAATGAAAGATTACATAT  
1621 GTACTATGACGAGAGTTTTACAAAGTCTCTCGATAGGTTGACTTACTTTCTAAGTGTATA 1680  
H D T A L K M F Q R A I Q L N E R F T Y  
GCACATACCTTTTGTGGCCACGAGTTTTCGGCATTTGGAAGAATTTCGAGGATGCAGAGAGA  
1681 CGTGTATGGGAAACACCGGTGCTCAAACGGCGTAACCTTCTTAAGCTCCTACGTCTCTCT 1740  
A H T L C G H E F A A L E E F E D A E R  
TGCTACCGGAAGGCTCTGGGCATAGATACGAGACACTATAATGCATGGTACGGTCTTTGGA  
1741 ACCATGGCCTTCCGAGACCCGTATCTATGCTCTGTGATATTACGTACCATGCCAGAACCT 1800  
C Y R K A L G I D T R H Y N A W Y G L G -

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1801 ATGACCTATCTTCGTCAGGAGAAATTCGAGTTTGCGCAGCATCAATTTCAACTGGCTCTC 1860  
TACTGGATAGAAGCAGTCCTCTTTAAGCTCAAACGCGTCGTAGTTAAAGTTGACCGAGAG  
M T Y L R Q E K F E F A Q H Q F Q L A L  
1861 CAAATAAATCCAAGATCTTCAGTCATCATGTGTTACTATGGAATTGCTTTGCATGAGTCA 1920  
GTTTATTTAGGTTCTAGAAGTCAGTAGTACACAATGATACCTTAACGAAACGTAACTCAGT  
Q I N P R S S V I M C Y Y G I A L H E S  
1921 AAGAGAAACGATGAGGCGTTGATGATGATGGAGAAGGCTGTACTCACTGATGCAAAGAAT 1980  
TTCTCTTTGCTACTCCGCAACTACTACTACCTCTTCCGACATGAGTGACTACGTTTCTTA  
K<sup>14/15</sup> R N D E A L M M M E K A V L T D A K N  
1981 CCGCTCCCCAAGTACTACAAGGCTCACATATTAACCAGCCTAGGTGATTATCACAAGCA 2040  
GGCGAGGGGTTTCATGATGTTCCGAGTGTATAATTGGTCCGATCCACTAATAGTGTTCCT  
P L P K Y Y K A H I L T S L G D Y H K A  
2041 CAGAAAGTTTTAGAAGAGCTCAAAGAATGTGCTCCTCAAGAAAGCAGTGTCCATGCATCG 2100  
GTCTTTCAAATCTTCTCGAGTTTCTTACACGAGGAGTTCTTTCGTACAGGTACGTAGC  
Q K V L E E L K E C A P Q E S S V H A S  
2101 CTTGGCAAAATATACAATCAGCTAAAGCAATACGACAAAGCCGTGTTACATTTCCGGCATT 2160  
GAACCGTTTTATATGTTAGTCGATTTTCGTTATGCTGTTTCGGCACAATGTAAAGCCGTAA  
L G K I Y N Q L K Q Y D K A V L H F G I  
2161 GCTTTGGAATTTAAGCCCTTCTCCATCTGATGCTGTCAAGATAAAGGCTTACATGGAGAGG 2220  
CGAAACCTAAATTCGGGAAGAGGTAGACTACGACAGTTCTATTTCCGAATGTACCTCTCC  
A L D L S P S P S D A V K I K<sup>15/16</sup> A Y M E R

2221 TTGATACTAACCGACGAGCGTGGTGACGGAGGAAATTTGTAGATTTATTTGTGCGGGTAA  
2280 AACCTATGATGGTCTGCTCGACCACTGCCTCCTTTTAACTCTTAAATACACCTCCTTTA

[illegible]

2341 CAGTCTTGTTGGACTTAACCCCTAAAAACAAAACCTGATTATATAAACTTACGAGGGTAAATTTAC  
-----  
GTGACAAACACCGATTGGGATTGTTGTTTGCATAATATATTTGAACTCTCCCAATTATATG 2400

2401 AGAAAATTGTATAGAGTTGGGTTTGAATTTTCTTTTCCAGTTGGAACCTTTTGT  
TCTTTTAACTATCTCAACCCAAACTTAAAGTAAAGAAAGGTTCAACCTTGAACA

[illegible][illegible]

# CDC27B Gene Structure

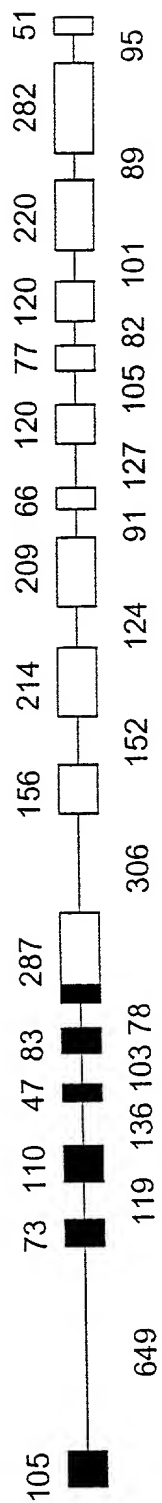


FIGURE 5

SEQ ID NO 6

Cdc27A1 1- MMENLLANCVQKNLNHFMTNAIFLCELLLAQFPSEVNLQLLARCYSNS  
Cdc27B 1- MEAMLV-DCVNSLRHFVYKNAIFMCEFLCAEFPSEVNLQLLATSYLQNN

SEQ ID NO 10

SEQ ID NO 6

Cdc27A1 51- QAYSAYVILKGSKTPOSRYLFAFSCEKLDLLGEAAALLP-CEDYAEVP  
Cdc27B 50- QAYSAYHLLKGTQMAQSRYLFAFSCEQMDLLNEAESALCPVNEPGAE-IP

SEQ ID NO 10

Cdc27A1 100- GGAAGHYLLGLIYRYSGRKNCISQOFRMALSFDPWCWEAYGELCSLGAAE  
Cdc27B 99- NGAAGHYLLGLIY----KKNAA-QQFKQSLTIDPLLWAAEELCILGAAE

SEQ ID NO 10

Cdc27A1 150- EASTVFCNVASQRLQKTCVEQRISFSEG-ATIDQ--ITDSKAL--KDTG  
Cdc27B 144- EATAVFGETAALSIQKQYMQO-LSTSLGLNTYNEERNSTSTKNTSSSEDYS

SEQ ID NO 10

Cdc27A1 194- LSQTEHIPGENQDDLKIMQQPGDIPPNTDRQLSTNGWDLNTPSPVLLQVM  
Cdc27B 193- PROSKHTQSHGLKDISGNFHSBGVNGGV----SNMSFY-NTPSPVAAQLS

Cdc27A1 244- D-APPPLLL NMRRPAV-EG-SLMS-----VHG-VRVRRRNEFFSE---  
Cdc27B 238- GIAPPPL-FRNFO-PAVANPNSLITDSSPKSTVNSTLOAPRRKEFVDEGKL

Cdc27A1 280- -ELSAEAQEESEG-RRRSARIAA-----RKKNPMSQSFGRKDSHWLHLSP  
Cdc27B 286- RKISGRFLFSDSGPRR-SSRLSADSGANINSSVATVSGNVNNAASKYLGGSK

SEQ ID NO 12

Cdc27A1 321- SESNYAPSLSSMIGKCRIQSSK-----EAIPD-TV-----TLNDPA  
Cdc27B 335- -----LSSLALRS-VTLRKGHSWANENM-DEGVRGEFPDDSRPNTAS

Cdc27A1 356- TTSGQSVSDTGSSVDDEEKNPSE--SSPDRFSLIS-GISEVLSILKILG  
Cdc27B 375- TTGSMASND----QEDETMSIGGIAMSSQT----ITIGVSEILNLLRTLGL

Cdc27A1 403- DGRHLHMYKQEAALLAYOKLSQKQYNTHWVLMQVGKAYFELDYFNADS  
Cdc27B 417- EGCRLSYMYRCQEAALDTYMKLPHKHYNTGWVLSQVGKAYFELIDYLEAEK

Cdc27A1 453- SETLAHQKYPYALEGMDTYSTVLYHLKEEMRLGYLAQELISVDRLSPESW  
Cdc27B 467- AERLARLASPYCLEGMDTYSTVLYHLKEDMKLSYLAQELISTDRLAQSW

Cdc27A1 503- CAVGNCYSLRKDHDITALKMFORAIQLNERFTYAHTLCGHEFAALEEFEDA  
Cdc27B 517- CAMGNCYSLQKDHETALKNFLRAVQLNPRFAYAHHTLCGHEYTTLDFENG

Cdc27A1 553- ERCYRKALGIDTRHYNAYGLGMTYLRQEKFEFAQHQFQLALQINPRSSV  
Cdc27B 567- MKSYQNALRVDTTRHYNAYGLGMIYLRQEKLEFSEHFERMAFLINPSSSV

Cdc27A1 603- IMCYGIALHESKRND EALMMMEKAVLTDKPNLPKYYKAHILTSIGDYH  
Cdc27B 617- IMSYLGTSLHALKRSEEALEIMEQAIVADRKNPLPMYOKANILVCLERLD

Cdc27A1 653- KAQVLEELKECAPQESSVHASL-GKIYNQLKQYDKAVLHFGIALDLSPS  
Cdc27B 667- EALEVLEELKEYAPSESSVYA-LMGRIYKRRNMEDKAMLHFGIALDMKPP

SEQ ID NO 7

Cdc27A1 702- PSDAVKIKAYMERLILPDELVTEENL  
Cdc27B 716- ATDVAAIKAAMEKLHVPDEIDESP

FIGURE 6

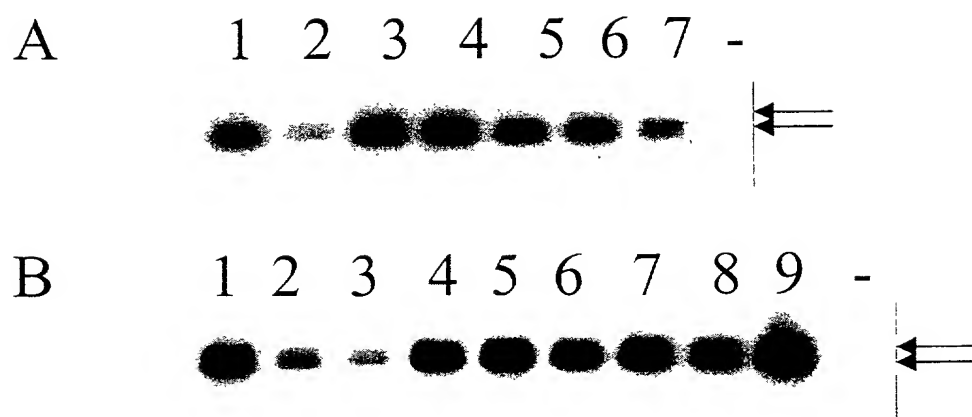


FIGURE 7



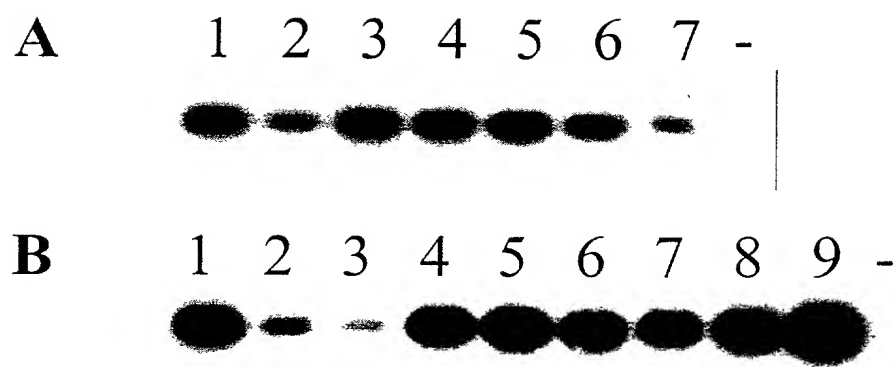


FIGURE 8